same species (14).--

Page 4, after line 15, replace the text entered in the amendment on July 24, 2000 with the following text:

--BRIEF DESCRIPTION OF THE DRAWING--

Fig. 1A illustrates the nucleotide and amino acid sequences of the synthetic gene (Bac 19) and the "native gene" (PF19) of *P. falciparum* described by Chang et al.

Fig. 1B illustrates the nucleotide and amino acid sequences of the synthetic gene (Bac 19) and the "native gene" (PF19) of the Uganda Palo Alto isolate of *P. falciparum.*

Fig 1C illustrates the PfMSP1$_{P19}$A recombinant protein sequence before cutting out the signal.

Fig. 1D illustrates the PfMSP1$_{P19}$A recombinant protein after cutting out the signal sequence.

Fig. 2A is an immunoblot using SDS-PAGE of the soluble recombinant PfMSP1$_{P19}$A antigen purified by immunoaffinity in the presence (reduced) or absence (non-reduced) of β-mercaptoethanol.

Fig. 2B is an immunoblot with human antiserum of recombinant purified MSP-1 P19 from *P. vivax* and *P. cynomolgi* under non-reduced (NR), reduced only in the charging medium (R) and irreversibly reduced (IR) conditions.

Fig. 3A is an immunoblot of the soluble PvMSPl$_{p42}$ recombinant antigen in the presence of protein fractions derived from merzoites of *P. falciparum* and separately isoelectric focusing in the presence (reduced) or absence (nonreduced) of β-mercaptoethanol.

Fig. 3B is a graph illustrating the results of an ELISA inhibition technique of *P. vivax* MSP-1 P42 and P19 antigens by the antiserum of individuals with an acquired immunity to *P. vivax*.

Fig. 4 recites nucleotide sequences. The underlined oligonucleotides originate from *P. vivax* and are used as primers in a PCR reaction. The lower portion of Fig.4 illustrates the percent identity between two isolates of *P. vivax* and *P. cynomolgi*.

Fig. 5 shows curves illustrating the variation in the measured parasitemia as the number of parasited red blood cells per microliter of blood as the function of time passed after infection. Curve A corresponds to the average values observed in three vaccinated monkeys and curve B corresponds to the average values in five controls.

Fig. 6A is a graph illustrating the parasitemia observed in non-vaccinated control animals as a function of time after injection.

Fig. 6BA is a graph illustrating the parasitemia observed in control animals which contained a saline solution also contain Freunds adjuvant as a function of time after injection.

Fig. 6C is a superposition of Figures 6A and 6B.

Fig. 6D is a graph illustrating parasitemia at the end of vaccination with p42 as a function of time.

Fig. 6E is a graph illustrating parasitemia in animals vaccinated with pl9 alone as a function of time.

Fig. 6F is a graph illustrating parasitemia in animals with a mixture of P42 and P19 as a function of time.

Fig. 6G is the data obtained to produce the graphs in Figs. 6A to 6F.

Fig. 7A is an immunoblot illustrating the in vivo response of monkeys to injections of pl9 with Freunds adjuvant (1), with alum (2) and in the form of liposomes (3).

Fig. 7B is an immunoblot illustrating the in vivo response of a squirrel monkey after three injections with p19 with Freunds adjuvant, with alum and in the form of liposomes.

Fig. 8A is a graph illustrating the percent parasitemia versus days post infection of six

monkeys, which were immunized with recombinant MSP-1 (pl9) six months earlier.

Fig. 8B is a graph illustrating the percent parasitemia versus days post infection of six monkeys that were immunized with normal saline and an adjuvant.

Fig. 8C is a graph illustrating the percent parasitemia versus days post infection of monkeys that were used as controls.

Fig. 8D is the data obtained to produce the graphs in Figs 8A to 8C.

Fig. 9A is a graph illustrating the percent parasitemia versus days post infection of 2 macaques immunized with recombinant pl9 and alum.

Fig. 9B is a graph illustrating the percent parasitemia versus days post infection of 2 macaques immunized with recombinant pl9 and alum.

Fig. 9C is a graph illustrating the percent parasitemia versus days post infection of a macaque immunized with pl9.

Fig. 9D is a graph illustrating the percent parasitemia versus days post infection of 3 control macaques immunized with physiological water and alum.

Fig. 9E is the data obtained to generate the graphs in Figs 9A to 9D.

Fig. 10A is a graph illustrating the percent parasitemia versus days post infection in a squirrel monkey immunized with MSP-1 pl9 and alum.

Fig. 10B is a graph illustrating the percent parasitemia versus days post infection in a squirrel monkey immunized with MSP-1 pl9 and Freunds.

Fig. 10C is a graph illustrating the percent parasitemia versus days post infection in a squirrel monkey immunized with MSP-1 pl9 with liposomes.

Fig. 10D is a graph illustrating the percent parasitemia versus days post infection in a squirrel monkey immunized with alum as the control.

Fig. 10E is a graph illustrating the percent parasitemia versus days post infection in a

squirrel monkey immunized with Freunds as the control.

Fig. 10F is a graph illustrating the percent parasitemia versus days post infection in a squirrel monkey immunized with liposomes as the control.

Fig. 10G is a graph illustrating the percent parasitemia versus days post infection in a squirrel monkey immunized with physiological water as the control.

Fig. 11A is a drawing of the backbone of $MSP1_{19}$ from *P. cynomolgi* showing disulfide bridges in bold line.

Fig. 11B is a drawing of the backbone of $MSP1_{19}$ showing positions of sequence differences between P. *cynomolgi and P. vivax.*

Fig. 11C is a drawing of the backbone of homology-modeled $MSP1_{19}$ of *P. falciparum* showing positions of sequence differences with *P. cynomolgi.*

Fig. 12 D is a NOESY spectrum of *P. vivax* $MSP1_{19}$.

Fig. 12 E is a NOESY spectrum of *P. vivax* $MSP1_{19}$.

Fig. 12 F is a NOESY spectrum of *P. vivax* $MSP1_{19}$.

Fig. 12.0a is a NOESY spectrum *of P.cynomolgi* $MSP1_{19}$.

Fig. 12.0b is a NOESY spectrum of *P. cynomolgi* $MSP1_{19}$.

Fig. 12.0c is a TOCSY spectrum of *P. cynomolgi* $MSP1_{19}$.

Fig. 12.1a is a NOESY spectrum of *P.vivax* $MSP1_{19}$.

Fig. 12.1b is a NOESY spectrum of *P. vivax* $MSP1_{19}$.

Fig. 12.1c is a TOCSY spectrum of *P. vivax* $MSP1_{19}$.

Fig. 12.2a is a NOESY spectrum of *P. falciparum* $MSP1_{19}$.

Fig. 12.2b is a NOESY spectrum of *P. falciparum* $MSP1_{19}$.

Fig. 12.2c is a TOCSY spectrum of *P. falciparum* $MSP1_{19}$.

E2 cancelled

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

Page 8, line 21 to page 9, line 12, replace the text in its entirety with the following:

The 19 kDa C-terminal fragment, the sequence of which is present in the active principle of the vaccine, can be limited to the sequence for the p19 itself, in the absence of any polypeptide sequence normally upstream of the p19 sequence in the corresponding MSP-1 protein. Clearly, though, the essential constiuent polypeptide sequence for the C-terminal side belonging to the 33 kDa (p33) N-terminal fragment still associated with the p19 in the corresponding p42, before natural cleavage of the latter, if the presence of this fragment does not modify the immunological properties of the active principle of the vaccine. As will be seen below, in particular in the description of the examples, the C-terminal sequences of the p33 in various strains of the same species of *Plasmodium* (see the C-terminal portion of the peptide sequences of "region III" in Figure 4 (SEQ ID NOS:11-14)) also have a degree of homology or substantial conservation of the sequence, for example on the order of at least 80%, in different varieties of *Plasmodiums* which are infectious for man, such that they do not fundamentally modify the vaccinating properties of the active principle (the sequence of which corresponds to region IV in Figure 4 (SEQ ID NOS:11-14)), in particular using the hypothesis which follows from this figure; that the presumed cleavage site between the p19 and region III of the p33 is located between the leucine and asparagines residues in a particularly well conserved region (LNVQTQ- SEQID NO:15).

Page 21, line 19 page 22, line 6, replace the text in its entirety with the following:

A 1200 base pair fragment was produced using a PCR reaction using the oligonucleotides underlined in **Figure 4** originating from *P. vivax* (see amino acids 1-6 and 373-380 of SEQ ID NO:13). The 5' oligonucleotide comprised an EcoRI restriction site and the 3' oligonucleotide comprises two synthetic TAA stop codons followed by a BglII

restriction site. This fragment was introduced by ligation and via these EcoRI and BglII sites into the $pVLLSV_{200}$ plasmid already containing the signal sequence for the MSP-1 protein of *P. vivax* (19). The new plasmid ($pVLSV_{200}C_{42}$) was used to analyze the DNA sequences.

The *P cynomolgi* (SEQ ID NO:11) and the corresponding *P. vivax* (SEQ ID NOS:12 and 13) sequences were aligned. The black arrows designate the presumed primary and secondary cleavage sites. They were determined by analogy with known sites in *P.falciparum* (27, 28). The vertical lines and horizontal arrows localize the limits of the four regions which were studied. Region 4 corresponded to the sequence coding for the *P. cynomolgi* p19. Glycosylation sites are boxed and the preserved cysteines are underlined. The lower portion of **Figure 4** shows the percentage identify between the two isolates of *P. vivax* and *P.cynomolgi*.

page 33, lines 12-16, replace the text in its entirety with the following:

In the present case, the most hypervariable regions are defined as region II or region II and all or part of region III, the portion of region II which is preferably deleted being that which is juxtaposed to region II (the conserved portion being located to the side of the C-terminal of p33, close to the p19). Regions II and III are illustrated in Figure 4 (SEQ ID NOS: 11-14).

Page 35, lines 6-19, replace the text in its entirety with the following:

--The invention relates also particularly to recombinant proteins, as obtainable in a baculovirus vector system:

-in a pure state

-substantially free of any other form of recombinant protein which, has the same peptide sequences, but which contains alternate conformations in the two EGF regions. This